

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=4; day=15; hr=13; min=10; sec=12; ms=469;]

=====

Application No: 10532681 Version No: 2.0

Input Set:**Output Set:**

Started: 2010-04-07 18:29:50.513
Finished: 2010-04-07 18:29:53.866
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 353 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2010-04-07 18:29:50.513
Finished: 2010-04-07 18:29:53.866
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 353 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)

SEQUENCE LISTING

<110> LUKYANOV, SERGEY A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10532681

<141> 2010-04-07

<160> 23

<170> PatentIn version 3.4

<210> 1

<211> 784

<212> DNA

<213> Phialidium sp.

<400> 1

```
gaactgataa aagaaatcat catcatgtct agtggagcac tgttgttcca cggaaagatc      60
ccatatgttg ttgagatgga gggaaatgtt gatggacaca cattctccat tagaggtaaa    120
ggttatggag atgcaagtgt tggtaaagtt gatgccaat tcatctgcac aactggagat      180
gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc      240
aaatatggtc cagaattaaa ggatttctac aagagttgca tgctgaagg ctatgtgcag      300
gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctgcgctga agttacattt      360
gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga      420
catgtgcttg gaaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga      480
gatcaggcta atcatggttt gaagtctgct ttcaaaatta tgcattgagat tactggatca      540
aaagaagact tcattgttgc agaccacacc caaatgaaca caccatttg tggtggacca      600
gtccatgtcc ctgaatacca tcatataaca taccatgtca ctctcagcaa agatgttact      660
gatcacaggg ataacatgag cttgggtgaa accgtacggg ctgtggattg cagaaaaaca      720
tatctttaa ttgtaaattt attttagtgg gaaaaccttt tgtcacgata tataccttta      780
ttat                                                                    784
```

<210> 2

<211> 234

<212> PRT

<213> Phialidium sp.

<400> 2

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 3
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-Y1 mutant of the phiYFP

<400> 3
atgcctagtg gagcactgtt gttccacgga aagatcccat atgttggtga gatggaggga 60
aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt 120
aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggtccaga attaaaggat 240
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggagtat ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttgaaa gaatcttgaa 420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480
tctgctttca aaattatgca tgagattact ggatcaaaag gagacttcat tgttgacagac 540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg 660
gttgaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 4
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 5

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M0 mutant of the phiYFP

<400> 5

```
atgcctagtg gagcactgtt gttccacgga aagatcccat atgttggtga gatggaggga      60
aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt    120
aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta    180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggtccaga attaaaggat    240
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg    300
gacggaaact ttaaaactcg cgetgaagtt acatttgaaa acggatctgt ttataaccga    360
gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa    420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaata tggtttgaag    480
tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgcacac    540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat    600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg    660
aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa                      705
```

<210> 6

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M0 mutant of the phiYFP

<400> 6

```
Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1              5              10              15
```

```
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
                20              25              30
```

```
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35              40              45
```

```
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50              55              60
```

```
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
```



```
<400> 7
atgtctagtg gagcactggt gttccacgga aagatcccat atggtgttga gatggaggga      60
aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt      120
aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta      180
```

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240
 ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg 300
 gacggaaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360
 gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420
 ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480
 tctgctttca aaatttgcca tgagattact ggatcaaaag gagacttcat tgttgcagac 540
 cacacccaaa tgaacacacc cattgggtggg ggaccagtcc atgtccctga ataccatcat 600
 atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660
 aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa 705

<210> 8

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> humanized version of the phiYFP-M1

<400> 9

atgagcagcg gcgccttgct gttccacggc aagatcccct acgtggtgga gatggagggc 60

aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc 120

aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc cctgcccctg gagcaccctg 180

gtgaccaccc tgacctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240

ttctacaaga gctgcatgcc cgatgggtac gtgcaggagc gcaccatcac cttcgagggc 300

gatggcaatt tcaagaccgc cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360

gtgaagctga atggccaggc cttcaagaag gatggccacg tgctgggcaa gaatctggag 420

ttcaatttca cccccactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480

agcgcccttca agatctgccca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac 600
atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
aaggagaccg tgcgcgccgt ggattgccgc aagacctacc tgtga 705

<210> 10

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> humanized version of the phiYFP-M1

<400> 10

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys

145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 11
<211> 1047
<212> DNA
<213> Anthomedusae species

<220>
<221> misc_feature
<223> hydromedusa 1 from sub-order Anthomedusae

<400> 11
cttttcttaa aaagaattca aaaaggacgg ttactagac atacttatac agctttactt 60
ataaaggaag aatgaatgt gatgcgttac aacagaggat tctgcagagt ttgcaaaat 120
ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaaccgt catacttggt 180
gcaatgacag aacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240
gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgtaatt 300
gaaggaaaat atgtttgtac agaaggagaa gtccctatct catgggtttc gctcatcacc 360
tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgattttttc 420
aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt 480
gttttagaaa cagcagctaa aattactatg gaaagtgggt caatagtga tagaataaat 540
gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600
cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac 660
atctatccaa caaagatgg tcactatggt gttgccgaca cacagcaagt aaatcgacca 720

attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat	780
ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca	840
tttgacgctg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag	900
ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa	960
tatatatttca aataaacttt ataaaattag gaatctttga atatataaac taaacctttt	1020
atttgtagaa taaaaataat taaagac	1047

<210> 12
 <211> 262
 <212> PRT
 <213> Anthomedusae species